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#2   OIPE

RAW SEQUENCE LISTING   DATE: 09/18/2001
PATENT APPLICATION: US/09/938,540   TIME: 11:03:25

Input Set : A:\ES.txt
Output Set: N:\CRF3\09182001\I938540.raw

ENTERED

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      3 <110> APPLICANT: Degussa AG
      5 <120> TITLE OF INVENTION: New nucleotide sequences which code for the ccpA1 gene
W-->  6 <130> FILE REFERENCE: 000059 BT
C-->  8 <140> CURRENT APPLICATION NUMBER: US/09/938,540
C-->  9 <141> CURRENT FILING DATE: 2001-08-27
     11 <160> NUMBER OF SEQ ID NOS: 4
     13 <170> SOFTWARE: PatentIn Ver. 2.1
     15 <210> SEQ ID NO: 1
     16 <211> LENGTH: 1600
     17 <212> TYPE: DNA
     18 <213> ORGANISM: Corynebacterium glutamicum
     20 <220> FEATURE:
     21 <221> NAME/KEY: CDS
     22 <222> LOCATION: (225)..(1388)
     23 <223> OTHER INFORMATION: ccpA1-Gen
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     28 agctctttcg cccattgagg tggaggggct gttttttcat gccgtaagga aagtgcaagt 120
     30 aagtgaaatc aagtggccta gatccattga cacttagact gtgacctagg cttgactttc 180
     32 gtgggggagt ggggataagt tcatcttaaa cacaatgcaa tcga ttg cat tta cgt 236
     33                                                 Met His Leu Arg
     34                                                  1
     36 tcc tta tcc cac aat agg ggt acc ttc cag aaa gtt ggt gag gag atg 284
     37 Ser Leu Ser His Asn Arg Gly Thr Phe Gln Lys Val Gly Glu Glu Met
     38   5                  10                  15                  20
     40 gct tcc gaa acc tcc agc ccg aag aag cgg gcc acc acg ctc aaa gac 332
     41 Ala Ser Glu Thr Ser Ser Pro Lys Lys Arg Ala Thr Thr Leu Lys Asp
     42                  25                  30                  35
     44 atc gcg caa gca aca cag ctt tca gtc agc acg gtg tcc cgg gca ttg 380
     45 Ile Ala Gln Ala Thr Gln Leu Ser Val Ser Thr Val Ser Arg Ala Leu
     46                  40                  45                  50
     48 gcc aac aac gcg agc att ccg gaa tcc aca cgc atc cga gtg gtt gaa 428
     49 Ala Asn Asn Ala Ser Ile Pro Glu Ser Thr Arg Ile Arg Val Val Glu
     50                  55                  60                  65
     52 gcc gct caa aag ctg aac tac cgt ccc aat gcc caa gct cgt gca ttg 476
     53 Ala Ala Gln Lys Leu Asn Tyr Arg Pro Asn Ala Gln Ala Arg Ala Leu
     54          70                  75                  80
     56 cgg aag tcg agg aca gac acc atc ggt gtc atc att cca aac att gag 524
     57 Arg Lys Ser Arg Thr Asp Thr Ile Gly Val Ile Ile Pro Asn Ile Glu
     58  85                  90                  95                  100
     60 aac cca tat ttc tcc tca cta gca gca tcg att caa aaa gct gct cgt 572
     61 Asn Pro Tyr Phe Ser Ser Leu Ala Ala Ser Ile Gln Lys Ala Ala Arg
     62                  105                 110                 115
     64 gaa gct ggg gtg tcc acc att ttg tcc aac tct gaa gaa aac cca gag 620
     65 Glu Ala Gly Val Ser Thr Ile Leu Ser Asn Ser Glu Glu Asn Pro Glu
     66                  120                 125                 130
     68 ctg ctt ggt cag act ttg gcg atc atg gat gac caa cgc ctc gat gga 668
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69 Leu Leu Gly Gln Thr Leu Ala Ile Met Asp Asp Gln Arg Leu Asp Gly
70          135                 140                 145
72 atc atc gtg gtg cca cac att cag tca gag gaa caa gtc act gac ttg   716
73 Ile Ile Val Val Pro His Ile Gln Ser Glu Glu Gln Val Thr Asp Leu
74          150                 155                 160
76 gtt aac agg gga gtg cca gta gtg ctg gca gac cgt agt ttt gtt aac   764
77 Val Asn Arg Gly Val Pro Val Val Leu Ala Asp Arg Ser Phe Val Asn
78 165                 170                 175                 180
80 tcg tct att cct tcg gtt acc tca gat cca gtt ccg ggc atg act gaa   812
81 Ser Ser Ile Pro Ser Val Thr Ser Asp Pro Val Pro Gly Met Thr Glu
82                  185                 190                 195
84 gct gtg gac tta ctc ctg gca gct gac gtg caa ttg ggc tac ctt gcc   860
85 Ala Val Asp Leu Leu Leu Ala Ala Asp Val Gln Leu Gly Tyr Leu Ala
86                  200                 205                 210
88 ggc ccg cag gat act tcc act ggt cag ctg cgt ctt aac act ttt gaa   908
89 Gly Pro Gln Asp Thr Ser Thr Gly Gln Leu Arg Leu Asn Thr Phe Glu
90          215                 220                 225
92 aga cta tgc gtg gac cgc ggc atc gtc gga gca tct gtc tat tac ggt   956
93 Arg Leu Cys Val Asp Arg Gly Ile Val Gly Ala Ser Val Tyr Tyr Gly
94          230                 235                 240
96 ggc tac cgc caa gaa tct gga tat gac ggc atc aag gtg ctg atc aag  1004
97 Gly Tyr Arg Gln Glu Ser Gly Tyr Asp Gly Ile Lys Val Leu Ile Lys
98 245                 250                 255                 260
100 cag gga gcc aat gcg att atc gct ggt gac tcc atg atg acc atc ggt 1052
101 Gln Gly Ala Asn Ala Ile Ile Ala Gly Asp Ser Met Met Thr Ile Gly
102                 265                 270                 275
104 gcg ttg ttg gct ctt cat gag atg aat ttg aag atc ggt gag gat gtg 1100
105 Ala Leu Leu Ala Leu His Glu Met Asn Leu Lys Ile Gly Glu Asp Val
106                 280                 285                 290
108 cag ctc att ggg ttt gat aac aac cca att ttc cgg ctg cag aat cca 1148
109 Gln Leu Ile Gly Phe Asp Asn Asn Pro Ile Phe Arg Leu Gln Asn Pro
110         295                 300                 305
112 ccg ctg agc atc att gac cag cac gta caa gag atc ggt aag cgt gcg 1196
113 Pro Leu Ser Ile Ile Asp Gln His Val Gln Glu Ile Gly Lys Arg Ala
114         310                 315                 320
116 ttt gag att ctg cag aag ctg atc aat ggg gac acc gcg caa aaa tct 1244
117 Phe Glu Ile Leu Gln Lys Leu Ile Asn Gly Asp Thr Ala Gln Lys Ser
118 325                 330                 335                 340
120 gtg gtg att cca acg cag ctc agc atc aat gga tca acg gcg gtt tcc 1292
121 Val Val Ile Pro Thr Gln Leu Ser Ile Asn Gly Ser Thr Ala Val Ser
122                 345                 350                 355
124 caa aag gcg gcc gca aag gca gca aaa gca gcc caa aaa gca gcc gcg 1340
125 Gln Lys Ala Ala Ala Lys Ala Ala Lys Ala Ala Gln Lys Ala Ala Ala
126                 360                 365                 370
128 aaa gcc gca cag aac acg caa cac gag gtg agc cta gat ggt gaa ctc 1388
129 Lys Ala Ala Gln Asn Thr Gln His Glu Val Ser Leu Asp Gly Glu Leu
130         375                 380                 385
132 tgaacaagcg cttcatcagc atgatcctgc accaatcctt cagttggata aagtctccaa 1448
134 gtcgtttggc ccagtcaacg tcattaatca agtgagcatc gatgttcgcc ctggcagggt 1508
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136 gcttgcgctg ttgggtgaaa atggtgcggg taaatctacg ctgatcaaga tgatgtcggg 1568
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142 <211> LENGTH: 388
143 <212> TYPE: PRT
144 <213> ORGANISM: Corynebacterium glutamicum
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151              20                  25                  30
153 Thr Leu Lys Asp Ile Ala Gln Ala Thr Gln Leu Ser Val Ser Thr Val
154          35                  40                  45
156 Ser Arg Ala Leu Ala Asn Asn Ala Ser Ile Pro Glu Ser Thr Arg Ile
157      50                  55                  60
159 Arg Val Val Glu Ala Ala Gln Lys Leu Asn Tyr Arg Pro Asn Ala Gln
160  65                  70                  75                  80
162 Ala Arg Ala Leu Arg Lys Ser Arg Thr Asp Thr Ile Gly Val Ile Ile
163                  85                  90                  95
165 Pro Asn Ile Glu Asn Pro Tyr Phe Ser Ser Leu Ala Ala Ser Ile Gln
166              100                 105                 110
168 Lys Ala Ala Arg Glu Ala Gly Val Ser Thr Ile Leu Ser Asn Ser Glu
169          115                 120                 125
171 Glu Asn Pro Glu Leu Leu Gly Gln Thr Leu Ala Ile Met Asp Asp Gln
172      130                 135                 140
174 Arg Leu Asp Gly Ile Ile Val Val Pro His Ile Gln Ser Glu Glu Gln
175 145                 150                 155                 160
177 Val Thr Asp Leu Val Asn Arg Gly Val Pro Val Val Leu Ala Asp Arg
178              165                 170                 175
180 Ser Phe Val Asn Ser Ser Ile Pro Ser Val Thr Ser Asp Pro Val Pro
181              180                 185                 190
183 Gly Met Thr Glu Ala Val Asp Leu Leu Leu Ala Ala Asp Val Gln Leu
184          195                 200                 205
186 Gly Tyr Leu Ala Gly Pro Gln Asp Thr Ser Thr Gly Gln Leu Arg Leu
187      210                 215                 220
189 Asn Thr Phe Glu Arg Leu Cys Val Asp Arg Gly Ile Val Gly Ala Ser
190 225                 230                 235                 240
192 Val Tyr Tyr Gly Gly Tyr Arg Gln Glu Ser Gly Tyr Asp Gly Ile Lys
193              245                 250                 255
195 Val Leu Ile Lys Gln Gly Ala Asn Ala Ile Ile Ala Gly Asp Ser Met
196          260                 265                 270
198 Met Thr Ile Gly Ala Leu Leu Ala Leu His Glu Met Asn Leu Lys Ile
199          275                 280                 285
201 Gly Glu Asp Val Gln Leu Ile Gly Phe Asp Asn Asn Pro Ile Phe Arg
202      290                 295                 300
204 Leu Gln Asn Pro Pro Leu Ser Ile Ile Asp Gln His Val Gln Glu Ile
205 305                 310                 315                 320
207 Gly Lys Arg Ala Phe Glu Ile Leu Gln Lys Leu Ile Asn Gly Asp Thr
208              325                 330                 335
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RAW SEQUENCE LISTING   DATE: 09/18/2001
PATENT APPLICATION: US/09/938,540   TIME: 11:03:25

        Input Set : **A:\ES.txt**
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210 Ala Gln Lys Ser Val Val Ile Pro Thr Gln Leu Ser Ile Asn Gly Ser
211   340   345   350
213 Thr Ala Val Ser Gln Lys Ala Ala Ala Lys Ala Ala Lys Ala Ala Gln
214   355   360   365
216 Lys Ala Ala Ala Lys Ala Ala Gln Asn Thr Gln His Glu Val Ser Leu
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219 Asp Gly Glu Leu
220 385
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225 <211> LENGTH: 20
226 <212> TYPE: DNA
227 <213> ORGANISM: Corynebacterium glutamicum
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Primer ccpAlintA
232 <400> SEQUENCE: 3
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237 <211> LENGTH: 20
238 <212> TYPE: DNA
239 <213> ORGANISM: Corynebacterium glutamicum
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Primer ccpAlintB
244 <400> SEQUENCE: 4
245 atccagattc ttggcggtag   20

VERIFICATION SUMMARY DATE: 09/18/2001
PATENT APPLICATION: **US/09/938,540** TIME: 11:03:26

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\09182001\I938540.raw**

L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Application Number
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date